

SEQUENCE LISTING

<110> Chadwick, Brian Paul
Frischauf, Anna-Maria

<120> METHODS AND COMPOSITIONS RELATING TO CD39-LIKE
POLYPEPTIDES AND NUCLEIC ACIDS

<130> 9598-066

<140> 09/240,639

<141> 1999-01-29

<160> 29

<170> PatentIn Ver. 2.0

<210> 1

<211> 2762

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (232)..(1599)

<400> 1

```
gtgggggtcgt atccgcgagg tggaggccgg ggtggcgccg gccggggcgg gggagcccaa 60
aagaccggct gccgcctgct ccccggaaaa gggcactcgt ctccgtgggt gtggcggagc 120
gcgcggtgca tggaatgggc tatgtgaatg aaaaaaggta tccgttatga aacttccaga 180
aaaacgagct acatttttca gcagccgcag cacggtcctt ggcaaacaag g atg aga 237
                                         Met Arg
                                         1
aaa ata tcc aac cac ggg agc ctg cgg gtg gcg aag gtg gca tac ccc 285
Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro
      5              10              15
ctg ggg ctg tgt gtg ggc gtg ttc atc tat gtt gcc tac atc aag tgg 333
Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp
      20              25              30
cac cgg gcc acc gcc acc cag gcc ttc ttc agc atc acc agg gca gcc 381
His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala
      35              40              45              50
ccg ggg gcc cgg tgg ggt cag cag gcc cac agc ccc ctg ggg aca gct 429
Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala
      55              60              65
gca gac ggg cac gag gtc ttc tac ggg atc atg ttt gat gca gga agc 477
Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser
      70              75              80
```

act ggc acc cga gta cac gtc ttc cag ttc acc cgg ccc ccc aga gaa 525
 Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu
 85 90 95

act ccc acg tta acc cac gaa acc ttc aaa gca gtg aag cca ggt ctt 573
 Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu
 100 105 110

tct gcc tat gct gat gat gtt gaa aag agc gct cag gga atc cgg gaa 621
 Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu
 115 120 125 130

cta ctg gat gtt gct aaa cag gac att ccg ttc gac ttc tgg aag gcc 669
 Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala
 135 140 145

acc cct ctg gtc ctc aag gcc aca gct ggc tta cgc ctg tta cct gga 717
 Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly
 150 155 160

gaa aag gcc cag aag tta ctg cag aag gtg aaa gaa gta ttt aaa gca 765
 Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala
 165 170 175

tcg cct ttc ctt gta ggg gat gac tgt gtt tcc atc atg aac gga aca 813
 Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr
 180 185 190

gat gaa ggc gtt tcg gcg tgg atc acc atc aac ttc ctg aca ggc agc 861
 Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser
 195 200 205 210

ttg aaa act cca gga ggg agc agc gtg ggc atg ctg gac ttg ggc gga 909
 Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly
 215 220 225

gga tcc act cag atc gcc ttc ctg cca cgc gtg gag ggc acc ctg cag 957
 Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln
 230 235 240

gcc tcc cca ccc ggc tac ctg acg gca ctg cgg atg ttt aac agg acc 1005
 Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr
 245 250 255

tac aag ctc tat tcc tac agc tac ctc ggg ctc ggg ctg atg tcg gca 1053
 Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala
 260 265 270

cgc ctg gcg atc ctg ggc ggc gtg gag ggg cag cct gct aag gat gga 1101
 Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly
 275 280 285 290

aag gag ttg gtc agc cct tgc ttg tct ccc agt ttc aaa gga gag tgg 1149
 Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp
 295 300 305

gaa cac gca gaa gtc acg tac agg gtt tca ggg cag aaa gca gcg gca 1197
 Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala
 310 315 320

agc ctg cac gag ctg tgt gct gcc aga gtg tca gag gtc ctt caa aac 1245
 Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn
 325 330 335

aga gtg cac agg acg gag gaa gtg aag cat gtg gac ttc tat gct ttc 1293
 Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe
 340 345 350

tcc tac tat tac gac ctt gca gct ggt gtg ggc ctc ata gat gcg gag 1341
 Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu
 355 360 365 370

aag gga ggc agc ctg gtg gtg ggg gac ttc gag atc gca gcc aag tac 1389
 Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr
 375 380 385

gtg tgt cgg acc ctg gag aca cag ccg cag agc agc ccc ttc tca tgc 1437
 Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys
 390 395 400

atg gac ctc acc tac gtc agc ctg cta ctc cag gag ttc ggc ttt ccc 1485
 Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro
 405 410 415

agg agc aaa gtg ctg aag ctc act cgg aaa att gac aat gtt gag acc 1533
 Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr
 420 425 430

agc tgg gct ctg ggg gcc att ttt cat tac atc gac tcc ctg aac aga 1581
 Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg
 435 440 445 450

cag aag agt cca gcc tca tagtggccga gccatccctg tccccgtcag 1629
 Gln Lys Ser Pro Ala Ser
 455

cagtgtctgt gtgtctgcat aaaccctcct gtcctggacg tgacttcacg ctgaggagcc 1689

acagcacagg ccgtgctggc actttctgca cactggctct gggacttgca gaaggcctgg 1749

tgctgccctg gcatcagcct cttccagtca catctggcca gagggctgtc tggacctggg 1809

ccctgctcaa tgccacctgt ctgcctgggc tccaagtggg caggaccagg acagaaccac 1869

aggcacacac tgagggggca gtgtggctcc ctgcctgtcc catcccatg ccccgctccg 1929

ggggctgtgg ctgctgctgt gcatgtccct gcgatgggag tcttgtctcc cagcctgtca 1989

gtttctcccc cagggcagag ctccccctcc tgcaagagtc tgggaggcgg tgcaggctgt 2049

cctggctgct ctggggaagc cgagggacag ccataacacc cccgggacag taggtctggg 2109

cggcaccact gggaactctg gacttgagtg tgtttctct tccctgggta tgaatgtgtg 2169

agttcaccca gaggcctgct ctcctcacac attgtgtggt ttgggggttaa tgatggaggg 2229
 agacacctct tcatagacgg caggtgcccc cctttcaggg agtctcccag catgggcgga 2289
 tgccggggcat gagctgctgt aaactatattg tggtgtgtgt gcttgagtga cgtctctgtc 2349
 gtgtgggtgc caagtgcttg tgtagaaact gtgttctgag ccccttttc tggacaccaa 2409
 ctgtgtcctg tgaatgtatc gctactgtga gctgttcccg cctagccagg gccatgtctt 2469
 aggtgcagct gtgccacggg tcagctgagc cacagtcccc gaaccaagct ctcggtgtct 2529
 cgggccacca tccgcccacc tcgggctgac cccacctcct ccatggacag tgtgagcccc 2589
 gggccgtgca tcctgctcag tgtggcgta gtgtcggggc tgagccctt gagctgcttc 2649
 agtgaatgta cagtgtccgg cagagctga acctcatgtg ttccactccc aataaaaggt 2709
 tgacaggggc ttctccttca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2762

<210> 2

<211> 456

<212> PRT

<213> Homo sapiens

<400> 2

Met Arg Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala
 1 5 10 15

Tyr Pro Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile
 20 25 30

Lys Trp His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg
 35 40 45

Ala Ala Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly
 50 55 60

Thr Ala Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala
 65 70 75 80

Gly Ser Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro
 85 90 95

Arg Glu Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro
 100 105 110

Gly Leu Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile
 115 120 125

Arg Glu Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp
 130 135 140

Lys Ala Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu
 145 150 155 160

Pro Gly Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe
 165 170 175
 Lys Ala Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn
 180 185 190
 Gly Thr Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr
 195 200 205
 Gly Ser Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu
 210 215 220
 Gly Gly Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr
 225 230 235 240
 Leu Gln Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn
 245 250 255
 Arg Thr Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met
 260 265 270
 Ser Ala Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys
 275 280 285
 Asp Gly Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly
 290 295 300
 Glu Trp Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala
 305 310 315 320
 Ala Ala Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu
 325 330 335
 Gln Asn Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr
 340 345 350
 Ala Phe Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp
 355 360 365
 Ala Glu Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala
 370 375 380
 Lys Tyr Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe
 385 390 395 400
 Ser Cys Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly
 405 410 415
 Phe Pro Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val
 420 425 430
 Glu Thr Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu
 435 440 445
 Asn Arg Gln Lys Ser Pro Ala Ser
 450 455

ttt agg ggt gct caa atc att tct ggg caa gaa gaa ggg gta tat gga	640
Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly	
175 180 185	
tgg att aca gcc aac tat tta atg gga aat ttc ctg gag aag aac ctg	688
Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu	
190 195 200	
tgg cac atg tgg gtg cac ccg cat gga gtg gaa acc acg ggt gcc ctg	736
Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu	
205 210 215	
gac tta ggt ggt gcc tcc acc caa ata tcc ttc gtg gca gga gag aag	784
Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys	
220 225 230	
atg gat ctg aac acc agc gac atc atg cag gtg tcc ctg tat ggc tac	832
Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr	
235 240 245 250	
gta tac acg ctc tac aca cac agc ttc cag tgc tat ggc cgg aat gag	880
Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu	
255 260 265	
gct gag aag aag ttt ctg gca atg ctc ctg cag aat tct cct acc aaa	928
Ala Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys	
270 275 280	
aac cat ctc acc aat ccc tgt tac cct cgg gat tat agc atc agc ttc	976
Asn His Leu Thr Asn Pro Cys Tyr Tyr Pro Arg Asp Tyr Ser Ile Ser Phe	
285 290 295	
acc atg ggc cat gta ttt gat agc ctg tgc act gtg gac cag agg cca	1024
Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro	
300 305 310	
gaa agt tat aac ccc aat gat gtc atc act ttt gaa gga act ggg gac	1072
Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp	
315 320 325 330	
cca tct ctg tgt aag gag aag gtg gct tcc ata ttt gac ttc aaa gct	1120
Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala	
335 340 345	
tgc cat gat caa gaa acc tgt tct ttt gat ggg gtt tat cag cca aag	1168
Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys	
350 355 360	
att aaa ggg cca ttt gtg gct ttt gca gga ttc tac tac aca gcc agt	1216
Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser	
365 370 375	
gct tta aat ctt tca ggt agc ttt tcc ctg gac acc ttc aac tcc agc	1264
Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser	
380 385 390	

acc tgg aat ttc tgc tca cag aat tgg agt cag ctc cca ctg ctg ctc 1312
Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu Leu
395 400 405 410

ccc aaa ttt gat gag gta tat gcc cgc tct tac tgc ttc tca gcc aac 1360
Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn
415 420 425

tac atc tac cac ttg ttt gtg aac ggt tac aaa ttc aca gag gag act 1408
Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr
430 435 440

tgg ccc caa ata cac ttt gaa aaa gaa gtg ggg aat agc agc ata gcc 1456
Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala
445 450 455

tgg tct ctt ggc tac atg ctc agc ctg acc aac cag atc cca gct gaa 1504
Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu
460 465 470

agc cct ctg atc cgt ctg ccc ata gaa cca cct gtc ttt gtg ggc acc 1552
Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr
475 480 485 490

ctc gct ttc ttc aca gtg gca gcc ttg ctg tgt ctg gca ttt ctt gca 1600
Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala
495 500 505

tac ctg tgt tca gca acc aga aga aag agg cac tcc gag cat gcc ttt 1648
Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe
510 515 520

gac cat gca gtg gat tct gac tgagccttca aagcagctcc tggagtccaa 1699
Asp His Ala Val Asp Ser Asp
525

tggctgctta gagtcagcct ggggtggcacc aggcaatgca ggtgaagtgg ctgccttcag 1759

gaaatacaac taactaaaat caaacaccta ggtcacgtgc ctctcaaata ctgatttctg 1819

ccacagcacc tcttgaggca tcccttggtt attctgtgca tattgttctt cagagacctc 1879

actaccacaca tgctgatcta ttggggaaca gagaagagac aggccactaa ggtcaggctc 1939

tttatattaa gttccccaga ggaagagtaa gttgagaagg tatcagttta atgttgaaga 1999

attgacctca gggctcagtt tccatttccc tccctcagta ttcttctctg caagataccc 2059

attaagcatt tcgccaatca gaatctcatt ttatagtttt tccattgggt ctttaactaa 2119

gactttcttg tagcaatctc gtaagcagtg aacccccctca gatcagtaga atatagtatc 2179

tgggggagaa gacttacttc cttcagggca gcagccacag ccaggcttct gtcatacagg 2239

tagatcccgaa agcacagaga cataaaaaag gtctcccaga aaactataga ccattctcca 2299

agtggaattc ccacttaggg ctctgggtcac tagattgcaa cctgtgtggt tgtcatcatc 2359

ctcatctcac cattgtattg ctatgccctc ccataaaaac acattgatcc ctagcaagat 2419
tattgcattc cagatttttac tgccttttgc aggcttttgc ttagcaaagg gctgactttc 2479
cattgttatc atggtgtata tttttttgtc accattccca caagtatact tgatgttgtc 2539
atagaacgaa catcctactc tatgattttac taaccaatta ctttcccaga tcatagacct 2599
ctctgcatag tagtcatagg tcttgacttt ggggaaagaa aaggaagctg caggaatatt 2659
tatctccaaa gtcgaatgag aaagaactcc agcaaatcca atggctacaa actaaaaatc 2719
agcattatct catattgctg tttcttagct gaatatggaa taaagaacta ttattttatt 2779
ttgaaaaaaaa aaaaaaaaaa 2797

<210> 4
<211> 529
<212> PRT
<213> Homo sapiens

<400> 4
Met Phe Thr Val Leu Thr Arg Gln Pro Cys Glu Gln Ala Gly Leu Lys
1 5 10 15
Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala Leu Val Val Leu Leu Val
20 25 30
Ser Ile Val Val Leu Val Ser Ile Thr Val Ile Gln Ile His Lys Gln
35 40 45
Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly Ile Val Leu Asp Ala Gly
50 55 60
Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln Trp Pro Ala Glu Lys Glu
65 70 75 80
Asn Asn Thr Gly Val Val Ser Gln Thr Phe Lys Cys Ser Val Lys Gly
85 90 95
Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro Gln Asp Val Pro Arg Ala
100 105 110
Phe Glu Glu Cys Met Gln Lys Val Lys Gly Gln Val Pro Ser His Leu
115 120 125
His Gly Ser Thr Pro Ile His Leu Gly Ala Thr Ala Gly Met Arg Leu
130 135 140
Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn Glu Val Leu Glu Ser Ile
145 150 155 160
Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp Phe Arg Gly Ala Gln Ile
165 170 175
Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly Trp Ile Thr Ala Asn Tyr
180 185 190

Leu Met Gly Asn Phe Leu Glu Lys Asn Leu Trp His Met Trp Val His
 195 200 205
 Pro His Gly Val Glu Thr Thr Gly Ala Leu Asp Leu Gly Gly Ala Ser
 210 215 220
 Thr Gln Ile Ser Phe Val Ala Gly Glu Lys Met Asp Leu Asn Thr Ser
 225 230 235 240
 Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr Val Tyr Thr Leu Tyr Thr
 245 250 255
 His Ser Phe Gln Cys Tyr Gly Arg Asn Glu Ala Glu Lys Lys Phe Leu
 260 265 270
 Ala Met Leu Leu Gln Asn Ser Pro Thr Lys Asn His Leu Thr Asn Pro
 275 280 285
 Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe Thr Met Gly His Val Phe
 290 295 300
 Asp Ser Leu Cys Thr Val Asp Gln Arg Pro Glu Ser Tyr Asn Pro Asn
 305 310 315 320
 Asp Val Ile Thr Phe Glu Gly Thr Gly Asp Pro Ser Leu Cys Lys Glu
 325 330 335
 Lys Val Ala Ser Ile Phe Asp Phe Lys Ala Cys His Asp Gln Glu Thr
 340 345 350
 Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys Ile Lys Gly Pro Phe Val
 355 360 365
 Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser Ala Leu Asn Leu Ser Gly
 370 375 380
 Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser Thr Trp Asn Phe Cys Ser
 385 390 395 400
 Gln Asn Trp Ser Gln Leu Pro Leu Leu Leu Pro Lys Phe Asp Glu Val
 405 410 415
 Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn Tyr Ile Tyr His Leu Phe
 420 425 430
 Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr Trp Pro Gln Ile His Phe
 435 440 445
 Glu Lys Glu Val Gly Asn Ser Ser Ile Ala Trp Ser Leu Gly Tyr Met
 450 455 460
 Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu Ser Pro Leu Ile Arg Leu
 465 470 475 480
 Pro Ile Glu Pro Pro Val Phe Val Gly Thr Leu Ala Phe Phe Thr Val
 485 490 495

Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala Tyr Leu Cys Ser Ala Thr
500 505 510

Arg Arg Lys Arg His Ser Glu His Ala Phe Asp His Ala Val Asp Ser
515 520 525

Asp

<210> 5
<211> 1998
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (247)..(1530)

<400> 5
gcgcgcgcgt tttccttggt cctgggtcaac aaagaaatgt ggagtgtctt ggctgaatcc 60
tcatacagac aagatcatta tgggtgctggt aggtaggact tgtatccaga tgtaagggtg 120
aaaaagtgat ataataaagg aaccaaggag aaaattcaga aggaaagaaa aaattgcctc 180
tgcaggtgtg cgagcaggat tgcttctgca acaaaagcct ccaccagcc acatcttggg 240
aaaaga atg gcc act tct tgg ggc aca gtc ttt ttc atg ctg gtg gta 288
Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val
1 5 10
tcc tgt gtt tgc agc gct gtc tcc cac agg aac cag cag act tgg ttt 336
Ser Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe
15 20 25 30
gag ggt atc ttc ctg tct tcc atg tgc ccc atc aat gtc agc gcc agc 384
Glu Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser
35 40 45
acc ttg tat gga att atg ttt gat gca ggg agc act gga act cga att 432
Thr Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile
50 55 60
cat gtt tac acc ttt gtg cag aaa atg cca gga cag ctt cca att cta 480
His Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu
65 70 75
gaa ggg gaa gtt ttt gat tct gtg aag cca gga ctt tct gct ttt gta 528
Glu Gly Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val
80 85 90
gat caa cct aag cag ggt gct gag acc gtt caa ggg ctc tta gag gtg 576
Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val
95 100 105 110

gcc aaa gac tca atc ccc cga agt cac tgg aaa aag acc cca gtg gtc	624
Ala Lys Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val	
115 120 125	
cta aag gca aca gca gga cta cgc tta ctg cca gaa cac aaa gcc aag	672
Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys	
130 135 140	
gct ctg ctc ttt gag gta aag gag atc ttc agg aag tca cct ttc ctg	720
Ala Leu Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu	
145 150 155	
gta cca aag ggc agt gtt agc atc atg gat gga tcc gac gaa ggc ata	768
Val Pro Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile	
160 165 170	
tta gct tgg gtt act gtg aat ttt ctg aca ggt cag ctg cat ggc cac	816
Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His	
175 180 185 190	
aga cag gag act gtg ggg acc ttg gac cta ggg gga gcc tcc acc caa	864
Arg Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln	
195 200 205	
atc acg ttc ctg ccc cag ttt gag aaa act ctg gaa caa act cct agg	912
Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg	
210 215 220	
ggc tac ctc act tcc ttt gag atg ttt aac agc act tat aag ctc tat	960
Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr	
225 230 235	
aca cat agt tac ttg gga ttt gga ttg aaa gct gca aga cta gca acc	1008
Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr	
240 245 250	
ctg gga gcc ctg gag aca gaa ggg act gat ggg cac act ttc cgg agt	1056
Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser	
255 260 265 270	
gcc tgt tta ccg aga tgg ttg gaa gca gag tgg atc ttt ggg ggt gtg	1104
Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val	
275 280 285	
aaa tac cag tat ggt ggc aac caa gaa ggg gag gtg ggc ttt gag ccc	1152
Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro	
290 295 300	
tgc tat gcc gaa gtg ctg agg gtg gta cga gga aaa ctt cac cag cca	1200
Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro	
305 310 315	
gag gag gtc cag aga ggt tcc ttc tat gct ttc tct tac tat tat gac	1248
Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp	
320 325 330	

cga gct gtt gac aca gac atg att gat tat gaa aag ggg ggt att tta 1296
 Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu
 335 340 345 350

aaa gtt gaa gat ttt gaa aga aaa gcc agg gaa gtg tgt gat aac ttg 1344
 Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu
 355 360 365

gaa aac ttc acc tca ggc agt cct ttc ctg tgc atg gat ctc agc tac 1392
 Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr
 370 375 380

atc aca gcc ctg tta aag gat ggc ttt ggc ttt gca gac agc aca gtc 1440
 Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val
 385 390 395

tta cag ctc aca aag aaa gtg aac aac ata gag acg ggc tgg gcc ttg 1488
 Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu
 400 405 410

ggg gcc acc ttt cac ctg ttg cag tct ctg ggc atc tcc cat 1530
 Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
 415 420 425

tgaggccaag tacttccttg gagacctgca ttgccaaca cctttttaag gggaggagag 1590

agcacttagt ttctgaacta gtctgggaca tcttggaact gagcctagag atttaggttt 1650

aattaatttt acacatctaa tgtgaactgc tgcctaacca ctcaagagta cacagctggc 1710

accagagcat cacagagagc cctgtgagcc aaaaagtata gttttggaac ttaaccttgg 1770

agtgagagcc cagggacagg tccttgaaa ccaaagaaaa atcgcatcttc aaccctttga 1830

gtgcctcatt ccaactgaata tttaaatttt cctcttaaat ggtaaaactga cttattgcaa 1890

tccaagacc catcaatata agtatattttt tcctccctat acagtgcctt gccaccctt 1950

atctgcaccc acctcccctg aaaaagagag aaaaaaaaaa aaaaaaaaaa 1998

<210> 6
 <211> 428
 <212> PRT
 <213> Homo sapiens

<400> 6
 Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
 1 5 10 15
 Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
 20 25 30
 Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
 35 40 45
 Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
 50 55 60

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
 65 70 75 80
 Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln
 85 90 95
 Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val Ala Lys
 100 105 110
 Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val Leu Lys
 115 120 125
 Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys Ala Leu
 130 135 140
 Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu Val Pro
 145 150 155 160
 Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile Leu Ala
 165 170 175
 Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His Arg Gln
 180 185 190
 Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr
 195 200 205
 Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr
 210 215 220
 Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr Thr His
 225 230 235 240
 Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly
 245 250 255
 Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys
 260 265 270
 Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr
 275 280 285
 Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro Cys Tyr
 290 295 300
 Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro Glu Glu
 305 310 315 320
 Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala
 325 330 335
 Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu Lys Val
 340 345 350
 Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Glu Asn
 355 360 365

Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr Ile Thr
 370 375 380
 Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
 385 390 395 400
 Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
 405 410 415
 Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
 420 425

<210> 7
 <211> 2119
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (205)..(1599)

<400> 7
 acgttgacac aggaatgaag agtgtattgg ctgaatcttc aagcagaggc gatattgacc 60
 atgtgctttt taaattggcc tgcgtgaccc gccacttgg tgtaaaagaa gaaccggcca 120
 aagggagggc ctgaaggacc tccacaggag tgtgagcagc actgcttcag caacaaagcc 180
 tcaggtccac atcttgggaa gaat atg gcc act tcc tgg ggg gct gtc ttc 231
 Met Ala Thr Ser Trp Gly Ala Val Phe
 1 5
 atg ctg atc ata gcc tgc gtt ggc agc act gtc ttc tac aga gaa cag 279
 Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln
 10 15 20 25
 cag acc tgg ttt gaa ggt gtc ttc ttg tct tcc atg tgc ccc att aat 327
 Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn
 30 35 40
 gtc agt gcc ggc acc ttt tat gga att atg ttt gat gcg ggc agc act 375
 Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr
 45 50 55
 gga gct cgg att cat gtt tac act ttt gtg cag aaa aca gca gga cag 423
 Gly Ala Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln
 60 65 70
 ctc ccc ttt ctg gaa ggt gaa att ttt gat tct gtg aag ccg gga ctt 471
 Leu Pro Phe Leu Glu Gly Glu Ile Phe Asp Ser Val Lys Pro Gly Leu
 75 80 85
 tct gct ttt gtg gat cag ccc aaa cag ggt gct gag act gtc cag gag 519
 Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Glu
 90 95 100 105

ctc ttg gag gtg gcc aaa gac tcg atc ccc aga agc cac tgg gaa agg	567
Leu Leu Glu Val Ala Lys Asp Ser Ile Pro Arg Ser His Trp Glu Arg	
110 115 120	
acc ccg gtg gtt ctg aaa gca acg gcc gga ctc cgt ttg ctg cct gag	615
Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu	
125 130 135	
cag aaa gcc cag gct ctg ctc ttg gag gta gag gag atc ttc aag aat	663
Gln Lys Ala Gln Ala Leu Leu Leu Glu Val Glu Glu Ile Phe Lys Asn	
140 145 150	
tca cct ttc ctg gtc cca gat ggc agc gtt agc atc atg gat ggg tcc	711
Ser Pro Phe Leu Val Pro Asp Gly Ser Val Ser Ile Met Asp Gly Ser	
155 160 165	
tat gaa ggc ata cta gcc tgg gtt acc gtg aac ttt cta aca ggt cag	759
Tyr Glu Gly Ile Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln	
170 175 180 185	
ctg cat ggt cgt ggc cag gag act gtg ggg acc ctt gac ctg ggg ggt	807
Leu His Gly Arg Gly Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly	
190 195 200	
gcc tcc acc caa atc acg ttt cta ccc cag ttt gag aaa acc ctg gaa	855
Ala Ser Thr Gln Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu	
205 210 215	
caa aca cct agg ggc tac ctc act tcc ttt gag atg ttt aac agc act	903
Gln Thr Pro Arg Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr	
220 225 230	
ttt aag ctc tat aca cat agt tac ttg gga ttt gga ctg aaa gct gca	951
Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala	
235 240 245	
aga ctg gca act ctg gga gcc ctg gaa gca aaa ggg act gat gga cat	999
Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His	
250 255 260 265	
acg ttt cga agt gcc tgt tta cca aga tgg ttg gaa gca gag tgg atc	1047
Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile	
270 275 280	
ttt ggg ggt gtg aaa tac cag tat ggt ggt aac caa gaa ggg gag atg	1095
Phe Gly Gly Val Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Met	
285 290 295	
ggc ttt gaa ccc tgc tat gcg gaa gtg ctg agg gta gta cag ggg aaa	1143
Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys	
300 305 310	
ctt cac cag cca gaa gaa gtc cga gga agc gcc ttc tac gct ttc tct	1191
Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser	
315 320 325	

tac tac tac gat cga gcc gct gac aca cac ttg atc gat tat gaa aag	1239
Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys	
330 335 340 345	
ggc ggg gtt tta aaa gtt gaa gat ttt gaa aga aaa gcc aga gaa gtg	1287
Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val	
350 355 360	
tgt gac aac ttg ggg agc ttc tcc tgc ggc agt cct ttc ctc tgc atg	1335
Cys Asp Asn Leu Gly Ser Phe Ser Ser Gly Ser Pro Phe Leu Cys Met	
365 370 375	
gac ctc act tac atc aca gcc ctg ttg aaa gat ggt ttg ggc ttt gcc	1383
Asp Leu Thr Tyr Ile Thr Ala Leu Leu Lys Asp Gly Leu Gly Phe Ala	
380 385 390	
gaa cgg cac cct ctt aca gct cac aaa gaa agt gaa caa cat aga gac	1431
Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp	
395 400 405	
tgg ttg ggc ctt ggg ggc cac ctt tca cct gct cca gtc tct ggg cat	1479
Trp Leu Gly Leu Gly Gly His Leu Ser Pro Ala Pro Val Ser Gly His	
410 415 420 425	
cac cag ctg agg cca agc tcc acc tct gaa gcc tgc att tct gaa cca	1527
His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro	
430 435 440	
gtt ttc tca cag gaa ggc gtg gac tca gag aca ttt tct gac ctc tct	1575
Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser	
445 450 455	
gga aaa gcc tgg ccc gaa acc cgt taactgggttt tataaggagg gagggggtttt	1629
Gly Lys Ala Trp Pro Glu Thr Arg	
460 465	
tagatgagtc ttgctcttga gcctagtgat ttgggcttca atgatttgca catctaattgt	1689
gaatagctcc taaccacttg gtgggtgcat ggctggcacc agactgtaaa tcttttgga	1749
ttctttgtac agagtcctgc aaaggaaaaa agagaaaagg tttggaactc catgctagat	1809
tgcgagttca gagacagtc cctggggacc aaagaacaat ctggtttcaa cccttgatg	1869
cctcattgct ttgaatggat tcatttttgc ttataagctg atttactgaa atcccataac	1929
ccatcaatgc tgtaattttt tttcttccta cccttattac attccctacc ctaaaagcct	1989
gggggaaata cctgggttttg cttcccatct ataattgaga aagagggggg aaaagatact	2049
gtattagaat ttgtgtgatc ctgtggcaca atagatcaac caaccattt aaagcttaaa	2109
aaaaaaaaa	2119

<210> 8
 <211> 465
 <212> PRT

<213> Mus musculus

<400> 8

Met Ala Thr Ser Trp Gly Ala Val Phe Met Leu Ile Ile Ala Cys Val
1 5 10 15
Gly Ser Thr Val Phe Tyr Arg Glu Gln Gln Thr Trp Phe Glu Gly Val
20 25 30
Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Gly Thr Phe Tyr
35 40 45
Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Ala Arg Ile His Val Tyr
50 55 60
Thr Phe Val Gln Lys Thr Ala Gly Gln Leu Pro Phe Leu Glu Gly Glu
65 70 75 80
Ile Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val Asp Gln Pro
85 90 95
Lys Gln Gly Ala Glu Thr Val Gln Glu Leu Leu Glu Val Ala Lys Asp
100 105 110
Ser Ile Pro Arg Ser His Trp Glu Arg Thr Pro Val Val Leu Lys Ala
115 120 125
Thr Ala Gly Leu Arg Leu Leu Pro Glu Gln Lys Ala Gln Ala Leu Leu
130 135 140
Leu Glu Val Glu Glu Ile Phe Lys Asn Ser Pro Phe Leu Val Pro Asp
145 150 155 160
Gly Ser Val Ser Ile Met Asp Gly Ser Tyr Glu Gly Ile Leu Ala Trp
165 170 175
Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly Arg Gly Gln Glu
180 185 190
Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln Ile Thr Phe
195 200 205
Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg Gly Tyr Leu
210 215 220
Thr Ser Phe Glu Met Phe Asn Ser Thr Phe Lys Leu Tyr Thr His Ser
225 230 235 240
Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr Leu Gly Ala
245 250 255
Leu Glu Ala Lys Gly Thr Asp Gly His Thr Phe Arg Ser Ala Cys Leu
260 265 270
Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val Lys Tyr Gln
275 280 285

Tyr Gly Gly Asn Gln Glu Gly Glu Met Gly Phe Glu Pro Cys Tyr Ala
290 295 300

Glu Val Leu Arg Val Val Gln Gly Lys Leu His Gln Pro Glu Glu Val
305 310 315 320

Arg Gly Ser Ala Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp Arg Ala Ala
325 330 335

Asp Thr His Leu Ile Asp Tyr Glu Lys Gly Gly Val Leu Lys Val Glu
340 345 350

Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu Gly Ser Phe
355 360 365

Ser Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Thr Tyr Ile Thr Ala
370 375 380

Leu Leu Lys Asp Gly Leu Gly Phe Ala Glu Arg His Pro Leu Thr Ala
385 390 395 400

His Lys Glu Ser Glu Gln His Arg Asp Trp Leu Gly Leu Gly Gly His
405 410 415

Leu Ser Pro Ala Pro Val Ser Gly His His Gln Leu Arg Pro Ser Ser
420 425 430

Thr Ser Glu Ala Cys Ile Ser Glu Pro Val Phe Ser Gln Glu Gly Val
435 440 445

Asp Ser Glu Thr Phe Ser Asp Leu Ser Gly Lys Ala Trp Pro Glu Thr
450 455 460

Arg
465

<210> 9

<211> 428

<212> PRT

<213> Homo sapiens

<400> 9

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
20 25 30

Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile His Val
50 55 60

Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu Glu Gly
65 70 75 80

Ala Leu Leu Lys Asp Gly Phe Gly Phe Ala Asp Ser Thr Val Leu Gln
385 390 395 400

Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu Gly Ala
405 410 415

Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His
420 425

<210> 10
<211> 455
<212> PRT
<213> P. sativum

<400> 10
Met Glu Leu Leu Ile Lys Leu Ile Thr Phe Leu Leu Phe Ser Met Pro
1 5 10 15

Ala Ile Thr Ser Ser Gln Tyr Leu Gly Asn Asn Leu Leu Thr Ser Arg
20 25 30

Lys Ile Phe Leu Lys Gln Glu Glu Ile Ser Ser Tyr Ala Val Val Phe
35 40 45

Asp Ala Gly Ser Thr Gly Ser Arg Ile His Val Tyr His Phe Asn Gln
50 55 60

Asn Leu Asp Leu Leu His Ile Gly Lys Gly Val Glu Tyr Tyr Asn Lys
65 70 75 80

Ile Thr Pro Gly Leu Ser Ser Tyr Ala Asn Asn Pro Glu Gln Ala Ala
85 90 95

Lys Ser Leu Ile Pro Leu Leu Glu Gln Ala Glu Asp Val Val Pro Asp
100 105 110

Asp Leu Gln Pro Lys Thr Pro Val Arg Leu Gly Ala Thr Ala Gly Leu
115 120 125

Arg Leu Leu Asn Gly Asp Ala Ser Glu Lys Ile Leu Gln Ser Val Arg
130 135 140

Asp Met Leu Ser Asn Arg Ser Thr Phe Asn Val Gln Pro Asp Ala Val
145 150 155 160

Ser Ile Ile Asp Gly Thr Gln Glu Gly Ser Tyr Leu Trp Val Thr Val
165 170 175

Asn Tyr Ala Leu Gly Asn Leu Gly Lys Lys Tyr Thr Lys Thr Val Gly
180 185 190

Val Ile Asp Leu Gly Gly Gly Ser Val Gln Met Ala Tyr Ala Val Ser
195 200 205

Lys Lys Thr Ala Lys Asn Ala Pro Lys Val Ala Asp Gly Asp Asp Pro
210 215 220

Tyr Ile Lys Lys Val Val Leu Lys Gly Ile Pro Tyr Asp Leu Tyr Val
 225 230 235 240
 His Ser Tyr Leu His Phe Gly Arg Glu Ala Ser Arg Ala Glu Ile Leu
 245 250 255
 Lys Leu Thr Pro Arg Ser Pro Asn Pro Cys Leu Leu Ala Gly Phe Asn
 260 265 270
 Gly Ile Tyr Thr Tyr Ser Gly Glu Glu Phe Lys Ala Thr Ala Tyr Thr
 275 280 285
 Ser Gly Ala Asn Phe Asn Lys Cys Lys Asn Thr Ile Arg Lys Ala Leu
 290 295 300
 Lys Leu Asn Tyr Pro Cys Pro Tyr Gln Asn Cys Thr Phe Gly Gly Ile
 305 310 315 320
 Trp Asn Gly Gly Gly Gly Asn Gly Gln Lys Asn Leu Phe Ala Ser Ser
 325 330 335
 Ser Phe Phe Tyr Leu Pro Glu Asp Thr Gly Met Val Asp Ala Ser Thr
 340 345 350
 Pro Asn Phe Ile Leu Arg Pro Val Asp Ile Glu Thr Lys Ala Lys Glu
 355 360 365
 Ala Cys Ala Leu Asn Phe Glu Asp Ala Lys Ser Thr Tyr Pro Phe Leu
 370 375 380
 Asp Lys Lys Asn Val Ala Ser Tyr Val Cys Met Asp Leu Ile Tyr Gln
 385 390 395 400
 Tyr Val Leu Leu Val Asp Gly Phe Gly Leu Asp Pro Leu Gln Lys Ile
 405 410 415
 Thr Ser Gly Lys Glu Ile Glu Tyr Gln Asp Ala Ile Val Glu Ala Ala
 420 425 430
 Trp Pro Leu Gly Asn Ala Val Glu Ala Ile Ser Ala Leu Pro Lys Phe
 435 440 445
 Glu Arg Leu Met Tyr Phe Val
 450 455

<210> 11
 <211> 454
 <212> PRT
 <213> Solanum tuberosum

<400> 11
 Met Leu Asn Gln Asn Ser His Phe Ile Phe Ile Ile Leu Ala Ile Phe
 1 5 10 15
 Leu Val Leu Pro Leu Ser Leu Leu Ser Lys Asn Val Asn Ala Gln Ile
 20 25 30

Pro Leu Arg Arg His Leu Leu Ser His Glu Ser Glu His Tyr Ala Val
 35 40 45
 Ile Phe Asp Ala Gly Ser Thr Gly Ser Arg Val His Val Phe Arg Phe
 50 55 60
 Asp Glu Lys Leu Gly Leu Leu Pro Ile Gly Asn Asn Ile Glu Tyr Phe
 65 70 75 80
 Met Ala Thr Glu Pro Gly Leu Ser Ser Tyr Ala Glu Asp Pro Lys Ala
 85 90 95
 Ala Ala Asn Ser Leu Glu Pro Leu Leu Asp Gly Ala Glu Gly Val Val
 100 105 110
 Pro Gln Glu Leu Gln Ser Glu Thr Pro Leu Glu Leu Gly Ala Thr Ala
 115 120 125
 Gly Leu Arg Met Leu Lys Gly Asp Ala Ala Glu Lys Ile Leu Gln Ala
 130 135 140
 Val Arg Asn Leu Val Lys Asn Gln Ser Thr Phe His Ser Lys Asp Gln
 145 150 155 160
 Trp Val Thr Ile Leu Asp Gly Thr Gln Glu Gly Ser Tyr Met Trp Ala
 165 170 175
 Ala Ile Asn Tyr Leu Leu Gly Asn Leu Gly Lys Asp Tyr Lys Ser Thr
 180 185 190
 Thr Ala Thr Ile Asp Leu Gly Gly Gly Ser Val Gln Met Ala Tyr Ala
 195 200 205
 Ile Ser Asn Glu Gln Phe Ala Lys Ala Pro Gln Asn Glu Asp Gly Glu
 210 215 220
 Pro Tyr Val Gln Gln Lys His Leu Met Ser Lys Asp Tyr Asn Leu Tyr
 225 230 235 240
 Val His Ser Tyr Leu Asn Tyr Gly Gln Leu Ala Gly Arg Ala Glu Ile
 245 250 255
 Phe Lys Ala Ser Arg Asn Glu Ser Asn Pro Cys Ala Leu Glu Gly Cys
 260 265 270
 Asp Gly Tyr Tyr Ser Tyr Gly Gly Val Asp Tyr Lys Val Lys Ala Pro
 275 280 285
 Lys Lys Gly Ser Ser Trp Lys Arg Cys Arg Arg Leu Thr Arg His Ala
 290 295 300
 Leu Lys Ile Asn Ala Lys Cys Asn Ile Glu Glu Cys Thr Phe Asn Gly
 305 310 315 320
 Val Trp Asn Gly Gly Gly Gly Asp Gly Gln Lys Asn Ile His Ala Ser
 325 330 335

Ser Phe Phe Tyr Asp Ile Gly Ala Gln Val Gly Ile Val Asp Thr Lys
340 345 350

Phe Pro Ser Ala Leu Ala Lys Pro Ile Gln Tyr Leu Asn Ala Ala Lys
355 360 365

Val Ala Cys Gln Thr Asn Val Ala Asp Ile Lys Ser Ile Phe Pro Lys
370 375 380

Thr Gln Asp Arg Asn Ile Pro Tyr Leu Cys Met Asp Leu Ile Tyr Glu
385 390 395 400

Tyr Thr Leu Leu Val Asp Gly Phe Gly Leu Asn Pro His Lys Glu Ile
405 410 415

Thr Val Ile His Asp Val Gln Tyr Lys Asn Tyr Leu Val Gly Ala Ala
420 425 430

Trp Pro Leu Gly Cys Ala Ile Asp Leu Val Ser Ser Thr Thr Asn Lys
435 440 445

Ile Arg Val Ala Ser Ser
450

<210> 12

<211> 473

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 12

Lys Thr Pro Glu Asp Ile Ser Ile Ile Pro Val Asn Asp Glu Pro Gly
1 5 10 15

Tyr Leu Gln Asp Ser Lys Thr Glu Gln Asn Tyr Pro Glu Leu Ala Asp
20 25 30

Ala Val Lys Ser Gln Thr Ser Gln Thr Cys Ser Glu Glu His Lys Tyr
35 40 45

Val Ile Met Ile Asp Ala Gly Ser Thr Gly Ser Arg Val His Ile Tyr
50 55 60

Lys Phe Asp Val Cys Thr Ser Pro Pro Thr Leu Leu Asp Glu Lys Phe
65 70 75 80

Asp Met Leu Glu Pro Gly Leu Ser Ser Phe Asp Thr Asp Ser Val Gly
85 90 95

Ala Ala Asn Ser Leu Asp Pro Leu Leu Lys Val Ala Met Asn Tyr Val
100 105 110

Pro Ile Lys Ala Arg Ser Cys Thr Pro Val Ala Val Lys Ala Thr Ala
115 120 125

Gly Leu Arg Leu Leu Gly Asp Ala Lys Ser Ser Lys Ile Leu Ser Ala
130 135 140

Val Arg Asp His Leu Glu Lys Asp Tyr Pro Phe Pro Val Val Glu Gly
 145 150 155 160
 Asp Gly Val Ser Ile Met Gly Gly Asp Glu Glu Gly Val Phe Ala Trp
 165 170 175
 Ile Thr Thr Asn Tyr Leu Leu Gly Asn Ile Gly Ala Asn Gly Pro Lys
 180 185 190
 Leu Pro Thr Ala Ala Val Phe Asp Leu Gly Gly Gly Ser Thr Gln Ile
 195 200 205
 Val Glu Glu Pro Thr Phe Pro Ile Asn Glu Lys Met Val Asp Gly Glu
 210 215 220
 His Lys Phe Asp Leu Lys Phe Gly Asp Glu Asn Tyr Thr Leu Tyr Gln
 225 230 235 240
 Phe Ser His Leu Gly Tyr Gly Leu Lys Glu Gly Arg Asn Lys Val Asn
 245 250 255
 Ser Val Leu Val Glu Asn Ala Leu Lys Asp Lys Ile Leu Lys Gly Cys
 260 265 270
 Asn Thr Lys Thr His Cys Leu Ser Ser Pro Cys Leu Pro Pro Lys Val
 275 280 285
 Asn Ala Thr Asn Glu Lys Val Thr Leu Glu Ser Lys Glu Thr Tyr Thr
 290 295 300
 Ile Asp Phe Ile Gly Pro Asp Glu Pro Ser Gly Ala Gln Cys Arg Phe
 305 310 315 320
 Leu Thr Asp Glu Ile Leu Asn Lys Asp Ala Gln Cys Gln Ser Pro Pro
 325 330 335
 Cys Ser Phe Asn Gly Val His Gln Pro Ser Leu Val Arg Thr Phe Lys
 340 345 350
 Glu Ser Asn Asp Ile Tyr Ile Phe Ser Tyr Phe Tyr Asp Arg Thr Thr
 355 360 365
 Arg Pro Leu Gly Met Pro Leu Ser Phe Thr Leu Asn Glu Leu Asn Asp
 370 375 380
 Leu Ala Arg Ile Val Cys Lys Gly Glu Glu Thr Trp Asn Ser Val Phe
 385 390 395 400
 Ser Gly Ile Ala Gly Ser Leu Asp Glu Leu Glu Ser Asp Ser His Phe
 405 410 415
 Cys Leu Asp Leu Ser Phe Gln Val Ser Leu Leu His Thr Gly Tyr Asp
 420 425 430
 Ile Pro Leu Gln Arg Glu Leu Arg Thr Gly Lys Lys Ile Ala Asn Lys
 435 440 445

Glu Ile Gly Trp Cys Leu Gly Ala Ser Leu Pro Leu Leu Lys Ala Asp
 450 455 460

Asn Trp Lys Cys Lys Ile Gln Ser Ala
 465 470

<210> 13
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 13
 Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr
 1 5 10 15

Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His
 20 25 30

Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val
 35 40 45

Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg
 50 55 60

Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr
 65 70 75 80

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu
 85 90 95

Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr
 100 105 110

Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly
 115 120 125

Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln
 130 135 140

Lys Thr Arg Trp Phe Ser Ile Val Pro
 145 150

<210> 14
 <211> 154
 <212> PRT
 <213> Rattus norvegicus

<400> 14
 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Asn Leu
 1 5 10 15

Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
 20 25 30

Gln Leu Leu Glu Glu Cys Gln Val Lys Gly Pro Gly Ile Ser Lys Tyr
 35 40 45

Ala Gln Lys Thr Asp Glu Ile Ala Ala Tyr Leu Ala Glu Cys Met Lys
50 55 60

Met Ser Thr Glu Arg Ile Pro Ala Ser Lys Gln His Gln Thr Pro Val
65 70 75 80

Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Lys
85 90 95

Gln Ser Ala Asp Glu Val Leu Ala Ala Val Ser Arg Ser Leu Lys Ser
100 105 110

Tyr Pro Phe Asp Phe Gln Gly Ala Lys Ile Ile Thr Gly Gln Glu Glu
115 120 125

Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Arg Phe Thr
130 135 140

Gln Glu Gln Ser Trp Leu Asn Phe Ile Ser
145 150

<210> 15

<211> 153

<212> PRT

<213> Homo sapiens

<400> 15

Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Met Phe
1 5 10 15

Ile Tyr Lys Trp Pro Ala Asp Lys Glu Asn Asp Thr Gly Ile Val Gly
20 25 30

Gln His Ser Ser Cys Asp Val Pro Gly Gly Gly Ile Ser Ser Tyr Ala
35 40 45

Asp Asn Pro Ser Gly Ala Ser Gln Ser Leu Val Gly Cys Leu Glu Gln
50 55 60

Ala Leu Gln Asp Val Pro Lys Glu Arg His Ala Gly Thr Pro Leu Tyr
65 70 75 80

Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Asn Leu Thr Asn Pro Glu
85 90 95

Ala Ser Thr Ser Val Leu Met Ala Val Thr His Thr Leu Thr Gln Tyr
100 105 110

Pro Phe Asp Phe Arg Gly Ala Arg Ile Leu Ser Gly Gln Glu Glu Gly
115 120 125

Val Phe Gly Trp Val Thr Ala Asn Tyr Leu Leu Glu Asn Phe Ile Lys
130 135 140

Tyr Gly Trp Val Gly Arg Trp Phe Arg
145 150

<210> 16
 <211> 150
 <212> PRT
 <213> Gallus gallus

<400> 16
 Phe Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ala Val
 1 5 10 15
 Phe Ile Tyr Lys Trp Pro Ala Asp Lys Glu Asn Asp Thr Gly Val Val
 20 25 30
 Ser Glu His Ser Met Cys Asp Val Glu Gly Pro Gly Ile Ser Ser Tyr
 35 40 45
 Ser Ser Lys Pro Pro Ala Ala Gly Lys Ser Leu Glu His Cys Leu Ser
 50 55 60
 Gln Ala Met Arg Asp Val Pro Lys Glu Lys His Ala Asp Thr Pro Leu
 65 70 75 80
 Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Thr Ile Ala Asp Pro
 85 90 95
 Pro Ser Gln Thr Cys Leu Ser Ala Val Met Ala Thr Leu Lys Ser Tyr
 100 105 110
 Pro Phe Asp Phe Gly Gly Ala Lys Ile Leu Ser Gly Glu Glu Glu Gly
 115 120 125
 Val Phe Gly Trp Ile Thr Ala Asn Tyr Leu Leu Glu Asn Phe Ile Lys
 130 135 140
 Arg Gly Trp Leu Gly Glu
 145 150

<210> 17
 <211> 148
 <212> PRT
 <213> Caenorhabditis elegans

<400> 17
 Ile Lys Tyr Gly Val Ile Cys Asp Ala Gly Ser Ser Gly Thr Arg Leu
 1 5 10 15
 Phe Val Tyr Thr Leu Lys Pro Leu Ser Gly Gly Leu Thr Asn Ile Asp
 20 25 30
 Thr Leu Ile His Glu Ser Glu Pro Val Val Lys Lys Val Thr Pro Gly
 35 40 45
 Leu Ser Ser Phe Gly Asp Lys Pro Glu Gln Val Val Glu Tyr Leu Thr
 50 55 60
 Pro Leu Leu Arg Phe Ala Glu Glu His Ile Pro Tyr Glu Gln Leu Gly
 65 70 75 80

Glu Thr Asp Leu Leu Ile Phe Ala Thr Ala Gly Met Arg Leu Leu Pro
85 90 95

Glu Ala Gln Lys Asp Ala Ile Ile Lys Asn Leu Gln Asn Gly Leu Lys
100 105 110

Ser Val Thr Ala Leu Arg Val Ser Asp Ser Asn Ile Arg Ile Ile Asp
115 120 125

Gly Ala Trp Glu Gly Ile Tyr Ser Trp Ile Ala Val Asn Tyr Ile Leu
130 135 140

Gly Arg Phe Asp
145

<210> 18
<211> 10
<212> RNA
<213> Mus musculus

<400> 18
aagaauaugg 10

<210> 19
<211> 10
<212> RNA
<213> Vertebrate

<400> 19
gccgccaugg 10

<210> 20
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
ccagactgta aatcttttgg 20

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
agggaatgta ataagggtag 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 22
ctgcttgagt gacgtctctg 20

<210> 23
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 23
cacatgaggt tcagctcgtg 20

<210> 24
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 24
gtgaagtggc tgccttcagg 20

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 25
cctttgactc gggactccag 20

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 26
gaactgctgc ctaaccactc 20

<210> 27
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 27
attgatgggt cttgggattg c 21

<210> 28
<211> 10
<212> RNA
<213> Homo sapiens

<400> 28
augugaauga 10

<210> 29
<211> 10
<212> RNA
<213> Homo sapiens

<400> 29
acaaggauga 10